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PATENT TRADEMARK OFFICE

Docket No: 3322/0H401

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Joanne M. MEYER, Rory BARRINGTON-MARTIN, Alexander PARKER, Glenn T. BARNES

Serial No.: 09/770,107 Art Unit: 1637

Confirmation No.: 5349

Filed: January 24, 2001 Examiner: Wilder, Cynthia B

For: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC DISORDERS, INCLUDING SCHIZOPHRENIA

MARK-UP AMENDMENT

Please amend the application as follows:

Please amend the specification pursuant to 37 C.F.R. 1.121 as follows:

Please amend the paragraph extending from page 111 lines 10-19 as follows:

PCR amplification products of the DISC1 and DISC2 genomic sequences that contain exon (including the intron/exon junction), 5'-UTR, 3'-UTR and regulatory (*e.g.*, 5'-promoter) sequences of the DISC1 and/or DISC2 genes were generated from genetic samples obtained from individuals of the populations described in

Example 1, *supra*. The primers used are provided in **FIGURE 4**. The table in **FIG. 4** describes primer sequence pairs (columns 3 and 4) for the identification/amplification of DISC1 and/or DISC2 variants, as well as the location (column [5] 6) and length (column [6] 7) of the amplified sequence. The PCR primers were chosen to amplify DISC1 and/or DISC2 sequences from about 150 to about 450 bp in length, which are preferred size ranges for mutation analysis by the SSCP and DHPLC methods described here.

Please amend the paragraph extending from page 115 lines 17-28 as follows:

Certain SNPs identified in **TABLE 6A**, above (*i.e.*, *disc08a, disc16a, disc18a, disc21a, disc22a* and *disc22b*) are located within an untranslated region (*i.e.*, the 5'-UTR or the 3'-UTR) of the DISC1 or DISC2 cDNA sequence and are not expected, therefore, to affect the amino acid sequence of a polypeptide encoded by the cDNA. However, other SNPs identified in **TABLE 6A** (*i.e.*, *disc01a*, *disc0[2]3a,* and *disc43a*) are located within the coding region of the indicated cDNA sequence and, further, change a codon of that coding sequence to one for a different amino acid residue. The *disc43a* mutation is silent, *i.e.*, the altered codon translates to the same amino acid as the wild-type codon. However, the cDNA sequences which comprise the *disc01a* and *disc0[2]3a* SNPs do encode an altered gene product. Specifically, the polypeptides encoded by these SNPs comprise amino acid residue substitutions. The specific amino acid residue substitutions encoded by each of these SNPs are indicated in **TABLE 6B**, below.

Please amend Figure 4 as shown in the attached mark-up: